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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/479,877 01/10/00 WOLF

M

EXAMINER

HM22/6212
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POETNER, V

ART UNIT

PAPER NUMBER

1645

DATE MAILED:

02/12/01

USAMRMC
STAFF JUDGE ADVOCATE
FORT DETRICK, MD

2001 FEB 15 PM 3:13

Commissioner of Patents and Trademarks



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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/479,877	1/10/2000	Wolf et al	

EXAMINER	
Portner	
ART UNIT	PAPER NUMBER
1645	5

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

2. Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ginny Portner whose telephone number is (703)308-7543. The examiner can normally be reached on Monday through Friday from 7:30 AM to 5:00 PM except for the first friday of each two week period.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith, can be reached on (703) 308-3909. The fax phone number for this group is (703) 308-4242.

The Group and/or Art Unit location of your application in the PTO will be Group Art Unit 1645. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to this Art Unit.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

LZS
LYNETTE R. F. SMITH
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

7. Other: additional sequences found

Applicant Must Provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wolf, Marcia K
Cassels, Fred J
Boedeker, Edgar C
- (ii) TITLE OF INVENTION: Transformed Bacteria Producing GS6
Antigens as Vaccines
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hendricks and Assoc
 - (B) STREET: P.O. Box 2509
 - (C) CITY: Fairfax
 - (D) STATE: VA
 - (E) COUNTRY: US
 - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/479,877
 - (B) FILING DATE: 10-JAN-2000
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hendricks, Glenna M
 - (B) REGISTRATION NUMBER: 32,535
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703/425-8405
 - (B) TELEFAX: 703/425-8406

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTGTAA CCAGTTGATA AAAATATATC ACGCTGGAA TGACGTGATG TATATAACGGA	60
GCAGCTATGT CGGAACAGAT ATTTTCCTAT CGGTATGCGT TGTGAGTAAG CGTAAAGCCA	120
ATGCTGTCTG TAACTCCTGA TCCTTGCAGA CTAAATTAGA GCTCCTTCTA AATTAGACGG	180
ATGGATAAAC CTACAGACTG GCGCTCTGGG TCTCGCCGGA TATTTCTAA TGAATTAAAG	240
CTTCATATGG TTGAACTGGC TTCGAAACCA AATGCCAATG TCGCACAACT GGCTCGGGAA	300
CATGGCGTTG ATAACAACCT GATTTTAAA TAGCTACGCC TCTGGCAAAG AGAAGGACGT	360
ATTTCTCGTA GAATGCCTCC AACTATTGTA GGCCCTACAG TACCACTGAG GTAGCCTGAA	420
TTTAAAGCCG AAGCGGTCAAG AACTGTTCTT GGTGTGAACG TAGCACTCAC CAATAAAAGC	480
ATCAATACGG TGCTCTGTTG ACACATTACG AATGTTATGT ATACAATAAA AATGATTATA	540
GCAATATTAA TGGTGTATA TGAAGAAAAC AATTGGTTTA ATTCTAATTC TTGCTTCATT	600
CGGCAGCCAT GCCAGAACAG AAATAGCGAC TAAAAACTTC CCAGTATCAA CGACTATTTC	660
AAAAAGTTT TTTGCACCTG AACACAGAAT ACAGCCTCT TTTGGTGAAGA ATGTTGGAAA	720
GGAAGGAGCT TTATTATTAA GTGTGAACCTT AACTGTTCTT GAAAATGTAT CCCAGGTAAC	780
GGTCTACCCCT GTTTATGATG AAGATTATGG GTTAGGACGA CTAGTAAATA CCGCTGATGC	840
TTCCCAATCA ATAATCTACC AGATTGTTGA TGAGAAAGGG AAAAAAATGT TAAAAGATCA	900
TGGTGCAGAG GTTACACCTA ATCAACAAAT AACTTTAAA GCGCTGAATT ATACTAGCGG	960
GGAAAAAAAAA ATATCTCCTG GAATATATAA CGATCAGGTT ATGGTTGGTT ACTATGTAAA	1020
CTAAATACTG GAAGTATGAT TATGTTGAAA AAAATTATT CGGCTATTGC ATTAATTGCA	1080
GGAACCTCCG GAGTGGTAAA TGCAGGAAAC TGGCAATATA AATCTCTGGA TGTAAATGTA	1140
AATATTGAGC AAAATTATATT TCCAGATATT GATTCCGCTG TTCGTATAAT ACCTGTTAAT	1200
TACGATTCCG ACCCGAAACT GGATTCACAG TTATATACGG TTGAGATGAC GATCCCTGCA	1260
GGTGTAAAGCG CAGTTAAAT CGCACCAACA GATAGTCTGA CATCTTCTGG ACAGCAGATC	1320
GGAAAGCTGG TTAATGTAAA CAATCCAGAT CAAAATATGA ATTATTATAT CAGAAAGGAT	1380
TCTGGCGCTG GTAACCTTAT GGCAGGACAA AAAGGATCCT TTCCTGTCAA AGAGAATACG	1440
TCATACACAT TCTCAGCAAT TTATACTGGT GGCGAATACC CTAATAGCGG ATATTGCT	1500

GGTACTTATG CAGGAAATT GACTGTATCA TTTTACAGCA ATTAAAAAAA GGCCGCATTA 1560
TTGCGGCCAT TGACGATACT GCTAGGCAAA AATATGAAAT CAAAGTTAAT TATACTATTG 1620
ACGTTAGTGC CATTTCATC TTTTCAACA GGAAATAATT TTGAAATAAA TAAGACACGA 1680
GTAATTTACT CTGACAGCAC ACCATCAGTT CAAATATCAA ATAATAAAGC ATATCCTTA 1740
ATTATTCAAA GCAATGTATG GGATGAAAGC AATAATAAA ATCATGACTT TATAGCAACA 1800
CCACCGATTT TTAAAATGGA AAGTGAAAGT CGGAATATAA TAAAATAAT TAAAACAAC 1860
ATTAATTGCG CGGACTCTCA GGAAAGTATG AGATGGTTAT GTATTGAATC AATGCCACCA 1920
ATAGAAAAAA GTACTAAAAT AAACAGAAAA GAAGGAAGGA CAGACAGTAT TAATATCAGC 1980
ATTCGGGGGT GCATTAAACT GATATATCGA CCTGCCAGTG TTCCGTCTCC TGTTTTAAT 2040
AATATAGTAG AAAAATTAAA ATGGCATAAA AATGGAAAGT ATCTTGTATT AAAAATAAT 2100
ACACCCTATT ACATTAGCTT TTCTGAGGTT TTTTTGATT CAGATAAAGT AAACAATGCA 2160
AAAGATATT TATATGTAAA ACCATACTCA GAGAAGAAAA TAGATATCAG CAACAGAATA 2220
ATAAAAAAA TCAAATGGGC TATGATTGAT GATGCTGGCG CAAAAACAAA ACTTTATGAA 2280
TCAATTAT TAAAAATCTC ATTACAGTAT ACAAAAACAT CAGATTACAG GCTTGCTTTT 2340
TTTGCTATTT ATATATCCTT TCTCAACCTC ATATGGAAAT GAACAATTAA GTTTGACTC 2400
ACGATTCCCA CCATCAGGTT ATAATTACTC TTTAAATAGT AACTTACCTC CTGAAGGTGA 2460
GTATCTGGTT GATATTTATA TTAACAAAAT AAAAAGGAG TCCGCGATTA TTCTTTTTA 2520
TATAAAAGGA AATAAACTTG TACCATGTTT ATCAAAAGAA AAAATTCAT CTTGGGTAT 2580
CAACATTAAT AATAACGACA ACACAGAGTG TGTAGAAACA AGTAAGGCAG GTATTAGTAA 2640
TATCAGCTTT GAGTTAGCT CTCTCGTTT GTTTATTGCT GTACCGAAAA ATCTTCTGTC 2700
TGAGATTGAT AAAATATCAT CAAAGGATAT AGATAACGGG ATTCACTGCTT TATTTTTAA 2760
TTATCAAGTA AATACAAGGC TAGCCAATAA TAAAATCGT TATGATTACA TTTCTGTTTC 2820
ACCAAATATA AATTATTTT CATGGCGGTT GCGTAATCTT TTTGAATTAA ACCAAAACAA 2880
CGATGAAAAA ACATGGGAAA GAAACTACAC TTATCTAGAA AAAAGTTTTT ATGATAAAAAA 2940
GCTAAACTTA GTCGTTGGTG AAAGTTATAC GAATTCAAAT GTTTATAATA ACTACTCTT 3000
TACTGGTATT TCAGTTCTA CAGATACAGA TATGTATACG CCAAGTAAA TCGATTATAC 3060
ACCAGAAATT CATGGAGTGG CTGATTCAAGA CTCTCAGATT ATTGTCAGGC AAGGCAACAC 3120

CATTATCATT	AATGAAAGTG	TTCCAGCCGG	ACCGTTCTCA	TTTCCAATAA	CCAATCTCAT	3180	
GTATACTGGG	GGGCAACTTA	ATGTGGAGAT	AACAGATATT	TATGGAAATA	AAAAACAATA	3240	
TACTGTCAAT	AATTCCCTCTC	TTCCTGTTAT	GAGAAAAGCG	GGACTAATGG	TATATAATTT	3300	
TATATCTGGG	AAATTAACAA	AAAAAAATAG	TGAGGATGGT	GATTTTTTA	CTCAAGGTGA	3360	
TATTAAC TAC	GGTACTCACT	ATAACAGCAC	ACTATT CGGT	GGATATCAGT	TTAGTAAAAA	3420	
TTATTTAAC	TTATCTACTG	GTATAGGCAC	TGATCTGGGA	TTTCTGGAG	CATGGCTACT	3480	
ACACGTTAGC	AGAAGTAATT	TTAAGAATAA	AAATGGATAT	AATATTAATC	TACAACAAAA	3540	
CACTCAGTTA	AGACCATTCA	ATGCCGGGGT	TAATTCGAT	TACGCATACA	GAAAAAAAAG	3600	
GTATGTGGAA	CTTTCCGACA	TTGGCTGGCA	TGGTAATTAA	TATAATCAAC	TTAAAAATAG	3660	
TTTTCTTTA	TCCTTGTCAA	AATCATTGAA	TAAATACGGA	AATTTCTCAC	TTGATTATAA	3720	
CAAAATGAAA	TACTGGGATA	ATGCGTATGA	TAGTAACTCA	ATGTCGATTC	GTTATTTTT	3780	
TAAATTCA	TG CGAGCAATGA	TTACAACAAA	TTGTTCTTTA	AATAAATATC	AATCTTATGA	3840	
AAAAAAAGAT	AAAAGATTAA	GTATTAATAT	ATCATTGCCT	TTAACCAAAG	ATTACGGGCA	3900	
CATATCTTCA	AACTATTCA	TTTCCAATGC	AAATACAGGA	ACGGCAACCA	GTTCTGTAGG	3960	
CTTAAACGGT	AGTTTTTTA	ATGACGCAAG	ATTAAACTGG	AACATT CAGC	AGAACAGAAC	4020	
GACCCGTAAC	AATGGATATA	CTGATAATAC	CAGTTACATA	GCAACCAGCT	ATGCCTCTCC	4080	
CTATGGCGTT	TTTACTGGTT	CATATT CAGG	ATCGAACAAAG	TATTCAAGCC	AGTTTTATT	4140	
TGCATCGGG	GGTATTGTT	TGCATAGCGA	TGGCGTAGCT	TTTACTCAA	AAGCCGGAGA	4200	
TACCTCTGCT	CTTGTCCGTA	TTGATAATAT	TTCTGATATA	AAAATTGGTA	ACACTCCTGG	4260	
TGTTTATACT	GGGTATAATG	GTTTGCTTT	AATTCCCTCAT	CTTCAGCCGT	TCAAAAAAAA	4320	
CACCATTAA	ATTAATGATA	AAGGAATTCC	AGACGGTATT	ACTCTTGCTA	ATATAAAAAA	4380	
ACAAGTTATC	CCATCACGAG	GAGCTATTGT	TAAAGTAAAA	TTTGATGCTA	AAAAAGGCAA	4440	
TGACATTTG	TTTAAGCTTA	CAACTAAAGA	TGGAAAACG	CCCCCATTAG	GAGCTATAGC	4500	
CCATGAAAAA	AATGGAAAAC	AGATTAATAC	GGGTATCGTT	GACGATGATG	GTATGCTTTA	4560	
TATGTCTGG	TTATCAGGG	CAGGGATTAT	TAATGTAACA	TGGAATGGAA	AAGTCTGTT	4620	
ATTTCC	TTTT	TCAGAAAAAG	ATATATCTAG	CAAACAATTA	TCTGTTGTAA	ATAAACAAATG	4680
TTAGGTAGTG	CATCCAATTA	GTAGAACATG	TGTTTTCGA	TAAACGCTCC	GATCTTTT	4740	

TCGTGGATCT CAACTGAGCG TGAGAAGCAG ATTGTTTAC GAGCCAACCG CTTAATGCGG	4800
GTGCGTAGCG TCAGATTATT ACGCTCAATG CGTTGGGTGA ATATTTGCC GGTCAGATGC	4860
TTATTCTTCG GTACC	4875

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCCGCATTA TTGCGGCC

18

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCGCATTA TTGATTGCGG CC

22

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACATT ACGAATGTTA TGTATACAAT AAAAATGATT ATAGCAATAT TAATGGTGT	60
ATATGAAGAA ACAATTGGT TTAATTCTAA TTCTTGCTTC ATTCCGGCAGC CATGCCAGAA	120
CAGAAATAGC GACTAAAAAC TTCCCACTAT CAACGACTAT TTCAAAAAGT TTTTTGCAC	180
CTGAACCACG AATACAGCCT TCTTTGGTG AAAATGTTGG AAAGGAAGGA GCTTTATTAT	240
TTAGTGTGAA CTTAACTGTT CCTGAAAATG TATCCCAGGT AACGGTCTAC CCTGTTATG	300
ATGAAGATTA TGGGTTAGGA CGACTAGTAA ATACCGCTGA TGCTTCCCAA TCAATAATCT	360
ACCAGATTGT TGATGAGAAA GGGAAAAAAA TGTTAAAAGA TCATGGTGCA GAGGTTACAC	420
CTAATCAACA AATAACTTT AAAGCGCTGA ATTATACTAG CGGGGAAAAAA AAAATATCTC	480
CTGGAATATA TAACGATCAG GTTATGGTTG GTTACTATGT AAACTAA	527

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Lys Thr Ile Gly Leu Ile Leu Ile Leu Ala Ser Phe Gly Ser			
1	5	10	15

His Ala Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr		
20	25	30

Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe		
35	40	45

Gly Glu Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu		
50	55	60

Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
65 70 75 80

Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln
85 90 95

Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys
100 105 110

Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
115 120 125

Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn
130 135 140

Asp Gln Val Met Val Gly Tyr Tyr Val Asn
145 150

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ile Ile Ser Ala Ile Ala Leu Ile Ala Gly Thr Ser
1 5 10 15

Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
20 25 30

Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
35 40 45

Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu
50 55 60

Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
65 70 75 80

Ala Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
85 90 95

Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
100 105 110

Asp Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro
115 120 125

Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
130 135 140

Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu
145 150 155 160

Thr Val Ser Phe Tyr Ser Asn
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Asn Phe Glu Ile Asn Lys Thr Arg Val Ile Tyr Ser Asp Ser Thr
1 5 10 15

Pro Ser Val Gln Ile Ser Asn Asn Lys Ala Tyr Pro Leu Ile Ile Gln
20 25 30

Ser Asn Val Trp Asp Glu Ser Asn Asn Lys Asn His Asp Phe Ile Ala
35 40 45

Thr	Pro	Pro	Ile	Phe	Lys	Met	Glu	Ser	Glu	Ser	Arg	Asn	Ile	Ile	Lys
50						55							60		
Ile	Ile	Lys	Thr	Thr	Ile	Asn	Leu	Pro	Asp	Ser	Gln	Glu	Ser	Met	Arg
65					70				75					80	
Trp	Leu	Cys	Ile	Glu	Ser	Met	Pro	Pro	Ile	Glu	Lys	Ser	Thr	Lys	Ile
				85					90					95	
Asn	Arg	Lys	Glu	Gly	Arg	Thr	Asp	Ser	Ile	Asn	Ile	Ser	Ile	Arg	Gly
			100					105						110	
Cys	Ile	Lys	Leu	Ile	Tyr	Arg	Pro	Ala	Ser	Val	Pro	Ser	Pro	Val	Phe
			115				120							125	
Asn	Asn	Ile	Val	Glu	Lys	Leu	Lys	Trp	His	Lys	Asn	Gly	Lys	Tyr	Leu
			130			135								140	
Val	Leu	Lys	Asn	Asn	Thr	Pro	Tyr	Tyr	Ile	Ser	Phe	Ser	Glu	Val	Phe
			145			150				155				160	
Phe	Asp	Ser	Asp	Lys	Val	Asn	Asn	Ala	Lys	Asp	Ile	Leu	Tyr	Val	Lys
			165				170							175	
Pro	Tyr	Ser	Glu	Lys	Ile	Asp	Ile	Ser	Asn	Arg	Ile	Ile	Lys	Lys	
			180				185							190	
Ile	Lys	Trp	Ala	Met	Ile	Asp	Asp	Ala	Gly	Ala	Lys	Thr	Lys	Leu	Tyr
			195				200							205	
Glu	Ser	Ile	Leu												
			210												

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Gln Phe Tyr Lys Lys Ser His Tyr Ser Ile Gln Lys His Gln
1 5 10 15

Ile Thr Gly Leu Leu Phe Leu Leu Phe Ile Tyr Pro Phe Ser Thr Ser
20 25 30

Tyr Gly Asn Glu Gln Phe Ser Phe Asp Ser Arg Phe Leu Pro Ser Gly
35 40 45

Tyr Asn Tyr Ser Leu Asn Ser Asn Leu Pro Pro Glu Gly Glu Tyr Leu
50 55 60

Val Asp Ile Tyr Ile Asn Lys Ile Lys Lys Glu Ser Ala Ile Ile Pro
65 70 75 80

Phe Tyr Ile Lys Gly Asn Lys Leu Val Pro Cys Leu Ser Lys Glu Lys
85 90 95

Ile Ser Ser Leu Gly Ile Asn Ile Asn Asn Asn Asp Asn Thr Glu Cys
100 105 110

Val Glu Thr Ser Lys Ala Gly Ile Ser Asn Ile Ser Phe Glu Phe Ser
115 120 125

Ser Leu Arg Leu Phe Ile Ala Val Pro Lys Asn Leu Leu Ser Glu Ile
130 135 140

Asp Lys Ile Ser Ser Lys Asp Ile Asp Asn Gly Ile His Ala Leu Phe
145 150 155 160

Phe Asn Tyr Gln Val Asn Thr Arg Leu Ala Asn Asn Lys Asn Arg Tyr
165 170 175

Asp Tyr Ile Ser Val Ser Pro Asn Ile Asn Tyr Phe Ser Trp Arg Leu
180 185 190

Arg Asn Leu Phe Glu Phe Asn Gln Asn Asn Asp Glu Lys Thr Trp Glu
195 200 205

Arg Asn Tyr Thr Tyr Leu Glu Lys Ser Phe Tyr Asp Lys Lys Leu Asn
210 215 220

Leu Val Val Gly Glu Ser Tyr Thr Asn Ser Asn Val Tyr Asn Asn Tyr
225 230 235 240

Ser Phe Thr Gly Ile Ser Val Ser Thr Asp Thr Asp Met Tyr Thr Pro
245 250 255

Ser Glu Ile Asp Tyr Thr Pro Glu Ile His Gly Val Ala Asp Ser Asp
260 265 270

Ser Gln Ile Ile Val Arg Gln Gly Asn Thr Ile Ile Ile Asn Glu Ser
275 280 285

Val Pro Ala Gly Pro Phe Ser Phe Pro Ile Thr Asn Leu Met Tyr Thr
290 295 300

Gly Gly Gln Leu Asn Val Glu Ile Thr Asp Ile Tyr Gly Asn Lys Lys
305 310 315 320

Gln Tyr Thr Val Asn Asn Ser Ser Leu Pro Val Met Arg Lys Ala Gly
325 330 335

Leu Met Val Tyr Asn Phe Ile Ser Gly Lys Leu Thr Lys Lys Asn Ser
340 345 350

Glu Asp Gly Asp Phe Phe Thr Gln Gly Asp Ile Asn Tyr Gly Thr His
355 360 365

Tyr Asn Ser Thr Leu Phe Gly Gly Tyr Gln Phe Ser Lys Asn Tyr Phe
370 375 380

Asn Leu Ser Thr Gly Ile Gly Thr Asp Leu Gly Phe Ser Gly Ala Trp
385 390 395 400

Leu Leu His Val Ser Arg Ser Asn Phe Lys Asn Lys Asn Gly Tyr Asn
405 410 415

Ile Asn Leu Gln Gln Asn Thr Gln Leu Arg Pro Phe Asn Ala Gly Val
420 425 430

Asn Phe Asp Tyr Ala Tyr Arg Lys Lys Arg Tyr Val Glu Leu Ser Asp
435 440 445

Ile Gly Trp His Gly Asn Leu Tyr Asn Gln Leu Lys Asn Ser Phe Ser
450 455 460

Leu Ser Leu Ser Lys Ser Leu Asn Lys Tyr Gly Asn Phe Ser Leu Asp
465 470 475 480

Tyr Asn Lys Met Lys Tyr Trp Asp Asn Ala Tyr Asp Ser Asn Ser Met
485 490 495

Ser Ile Arg Tyr Phe Phe Lys Phe Met Arg Ala Met Ile Thr Thr Asn
500 505 510

Cys Ser Leu Asn Lys Tyr Gln Ser Tyr Glu Lys Lys Asp Lys Arg Phe
515 520 525

Ser Ile Asn Ile Ser Leu Pro Leu Thr Lys Asp Tyr Gly His Ile Ser
530 535 540

Ser Asn Tyr Ser Phe Ser Asn Ala Asn Thr Gly Thr Ala Thr Ser Ser
545 550 555 560

Val Gly Leu Asn Gly Ser Phe Phe Asn Asp Ala Arg Leu Asn Trp Asn
565 570 575

Ile Gln Gln Asn Arg Thr Thr Arg Asn Asn Gly Tyr Thr Asp Asn Thr
580 585 590

Ser Tyr Ile Ala Thr Ser Tyr Ala Ser Pro Tyr Gly Val Phe Thr Gly
595 600 605

Ser Tyr Ser Gly Ser Asn Lys Tyr Ser Ser Gln Phe Tyr Ser Ala Ser
610 615 620

Gly Gly Ile Val Leu His Ser Asp Gly Val Ala Phe Thr Gln Lys Ala
625 630 635 640

Gly Asp Thr Ser Ala Leu Val Arg Ile Asp Asn Ile Ser Asp Ile Lys
645 650 655

Ile Gly Asn Thr Pro Gly Val Tyr Thr Gly Tyr Asn Gly Phe Ala Leu
660 665 670

Ile Pro His Leu Gln Pro Phe Lys Lys Asn Thr Ile Leu Ile Asn Asp
675 680 685

Lys Gly Ile Pro Asp Gly Ile Thr Leu Ala Asn Ile Lys Lys Gln Val
690 695 700

Ile Pro Ser Arg Gly Ala Ile Val Lys Val Lys Phe Asp Ala Lys Lys
705 710 715 720

Gly Asn Asp Ile Leu Phe Lys Leu Thr Thr Lys Asp Gly Lys Thr Pro
725 730 735

Pro Leu Gly Ala Ile Ala His Glu Lys Asn Gly Lys Gln Ile Asn Thr
740 745 750

Gly Ile Val Asp Asp Asp Gly Met Leu Tyr Met Ser Gly Leu Ser Gly
755 760 765

Thr Gly Ile Ile Asn Val Thr Trp Asn Gly Lys Val Cys Ser Phe Pro
770 775 780

Phe Ser Glu Lys Asp Ile Ser Ser Lys Gln Leu Ser Val Val Asn Lys
785 790 795 800

Gln Cys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser
1 5 10 15

Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly Glu
20 25 30

Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr Val
35 40 45

Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp
50 55 60

Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser Ile
65 70 75 80

Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp His
85 90 95

Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn
100 105 110

Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp Gln
115 120 125

Val Met Val Gly Tyr Tyr Val Asn
130 135

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln
1 5 10 15

Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn
20 25 30

Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met
35 40 45

Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser
50 55 60

Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn
65 70 75 80

Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly
85 90 95

Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr
100 105 110

Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser
115 120 125

Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr
130 135 140

Ser Asn
145